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**BioInformatics & Molecular Analysis Section (BIMAS)**



## HLA Peptide Binding Predictions

**Function:** Rank potential 8-mer, 9-mer, or 10-mer peptides based on a predicted half-time of dissociation to HLA class I molecules. The analysis is based on coefficient tables deduced from the published literature by Dr. Kenneth Parker [kparker@atlas.niaid.nih.gov](mailto:kparker@atlas.niaid.nih.gov), NIAID, NIH.

Another web site for predicting which peptides bind to MHC molecules is SYFPEITHI, developed by Hans-Georg Rammensee's lab.

### Analysis Options:

#### HLA molecule

A1	▲
<b>A_0201</b>	
A_0205	
A24	
A3	▼

#### n-mers

9	▼
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Results Limited by: ☒ Explicit Number ☐ Predicted  $T_{(1/2)} \geq$

20	▼
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100	▼
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Please enter or paste an AA sequence to analyze (most formats accepted):

		▲
		▼
◀		▶

☒ Echo input sequence (generally recommended)

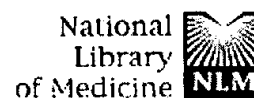
Credits: WWW implementation by Ronald Taylor of BIMAS / CBEL / CIT / NIH

If you use results from this analysis in published research, please cite:

*Parker, K. C., M. A. Bednarek, and J. E. Coligan. 1994. Scheme for ranking potential HLA-A2 binding peptides based on independent binding of individual peptide side-chains. J. Immunol. 152:163.*



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☐ 1: *AIDS Res Hum Retroviruses* 1997 May 1;13(7):529-31

Books, LinkOut

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**An interactive Web site providing major histocompatibility ligand predictions: application to HIV research.****De Groot AS, Jesdale BM, Szu E, Schafer JR, Chiczy RM, Deocampo G**

TB/HIV Research Laboratory, Brown University School of Medicine, Providence, Rhode Island 02912, USA.

Related Resources

EpiMatrix/HIV, a tool that is currently available on the World Wide Web, enables researchers to screen HIV proteins for potential MHC ligands. We have performed a comparison of EpiMatrix predictions to 158 published allotype-specific HLA-associated peptides (MHC ligands) derived from 133 proteins. The top 10 ranked EpiMatrix predictions for each of the 158 HLA allotype-protein pairs were selected for comparison with these published ligands. EpiMatrix correctly identified 134 of 158 published ligands (85%). The algorithm is now available for use by the HIV research community at the URL <http://www.EpiMatrix.com/HIV>.

PMID: 9135870

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